- (1) GENERAL INFORMATION:
- (i) APPLICANT: Barbas III, Carlos F. Gottesfeld, Joel M. Wright, Peter E.
- (ii) TITLE OF INVENTION: ZINC FINGER PROTEIN DERIVATIVES AND METHODS THEREFOR
- (iii) NUMBER OF SEQUENCES: 62
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Fish & Richardson P.C.
 - (B) STREET: 4225 Executive Square, Suite 1400
 - (C) CITY: La Jolla
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 92037
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: Windows 95
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0b
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/863,813
 - (B) FILING DATE: 27-MAY-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/676,318
 - (B) FILING DATE: 18-JUL-1996
 - (A) APPLICATION NUMBER: 08/183,119
 - (B) FILING DATE: 18-JAN-1996
 - (A) APPLICATION NUMBER: US95/00829
 - (B) FILING DATE: 18-JAN-1995
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Haile, Lisa A., Ph.D.
 - (B) REGISTRATION NUMBER: 38,347
 - (C) REFERENCE/DOCKET NUMBER: 08401/010001
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 619/678-5070
 - (B) TELEFAX: 619/678-5099
 - (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (B) LOCATION: 1...1
 - (D) OTHER INFORMATION: wher Xaa at position is Tyr or Phe

- (B) LOCATION: 2, 4-7, 9-11, 13-17, 19, 22-25, and 27-32
 (D) OTHER INFORMATION: where Xaa at the above positions is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val; Xaa at positions 6 or 7 may be missing; Xaa at position 25 may be missing; Xaa at positions 29, 30, 31, or 32 may be missing
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

- (2) INFORMATION FOR SEQ ID NO:2:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: ZF
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGAAACTGC TCGAGCCCTA TGCTTGCCCT GTCGAG

36

- (2) INFORMATION FOR SEQ ID NO:3:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: ZR
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAGGAGGAGG AGACTAGTGT CCTTCTGTCT TAAATGGATT TTGGT

45

- (2) INFORMATION FOR SEQ ID NO:4:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 273 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: zif268Xho-Spe
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 1...273

| | () | i) S | EQUE | ENCE | DESC | RIPT | : NOI | SEÇ |] ID | NO:4 | : | | | | | |
|------------------|------------------|------------------|------------------|-----------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|-----|
| CTC Leu 1 | GAG Glu | CCC Pro | TAT Tyr | GCT Ala 5 | TGC Cys | CCT Pro | GTC Val | GAG Glu | TCC Ser 10 | TGC Cys | GAT Asp | CGC Arg | CGC Arg | TTT Phe 15 | TCT Ser | 48 |
| CGC Arg | TCG Ser | GAT Asp | GAG Glu 20 | CTT Leu | ACC Thr | CGC Arg | CAT His | ATC Ile 25 | CGC Arg | ATC Ile | CAC His | ACA Thr | GGC Gly 30 | CAG Gln | AAG Lys | 96 |
| CCC Pro | TTC Phe | CAG Gln 35 | TGT Cys | CGA Arg | ATA Ile | TGC Cys | ATG Met 40 | CGT Arg | AAC Asn | TTC Phe | AGT Ser | CGT Arg 45 | AGT Ser | GAC Asp | CAC His | 144 |
| CTT Leu | ACC Thr 50 | ACC Thr | CAC His | ATC Ile | CGC Arg | ACC Thr 55 | CAC His | ACA Thr | GGC Gly | GAG Glu | AAG Lys 60 | CCT Pro | TTT Phe | GCC Ala | TGT Cys | 192 |
| GAC Asp 65 | ATT Ile | TGT Cys | GGG Gly | AGG Arg | AAG Lys 70 | TTT Phe | GCC Ala | AGG Arg | AGT Ser | GAT Asp 75 | GAA Glu | CGC Arg | AAG Lys | AGG Arg | CAT His 80 | 240 |
| ACC Thr | AAA Lys | ATC Ile | CAT His | TTA Leu | AGA Arg | CAG Gln | AAG Lys | GAC Asp | ACT Thr | AGT Ser | | | | | | 273 |

- (2) INFORMATION FOR SEQ ID NO:5:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 91 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Leu Glu Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser 10 Arg Ser Asp Glu Leu Thr Arg His Ile Arg Ile His Thr Gly Gln Lys 25 20 Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp His 35 40 Leu Thr Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys 60 55 50 Asp Ile Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys Arg His 80 75 70 65 Thr Lys Ile His Leu Arg Gln Lys Asp Thr Ser 85

- (2) INFORMATION FOR SEQ ID NO:6:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: FTX3

| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6: | |
|--|----|
| GCAATTAACC CTCACTAAAG GG | 22 |
| (2) INFORMATION FOR SEQ ID NO:7: | |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear | |
| (ii) MOLECULE TYPE: Genomic DNA | |
| (vii) IMMEDIATE SOURCE: (B) CLONE: BZF3 | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7: | |
| GGCAAACTTC CTCCCACAAA T | 21 |
| (2) INFORMATION FOR SEQ ID NO:8: | |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 60 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear | |
| (ii) MOLECULE TYPE: Genomic DNA | : |
| (vii) IMMEDIATE SOURCE: (B) CLONE: ZF36K | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8: | |
| ATTTGTGGGA GGAAGTTTGC CNNKAGTNNK NNKNNKNNKN NKCATACCAA AATCCATTTA | 60 |
| (2) INFORMATION FOR SEQ ID NO:9: | |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear | |
| (ii) MOLECULE TYPE: Genomic DNA | |
| (vii) IMMEDIATE SOURCE: (B) CLONE: R3B | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9: | |
| TTGATATTCA CAAACGAATG G | 21 |
| (2) INFORMATION FOR SEQ ID NO:10: | |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear | |
| (ii) MOLECULE TYPE: Genomic DNA | |
| | |

| (B) CLONE: ZFNsi-B | |
|--|----------|
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10: | |
| CATGCATATT CGACACTGGA A | 21 |
| (2) INFORMATION FOR SEQ ID NO:11: | |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 66 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear | |
| (ii) MOLECULE TYPE: Genomic DNA | |
| (vii) IMMEDIATE SOURCE: (B) CLONE: ZF2r6F | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11: | |
| CAGTGTCGAA TATGCATGCG TAACTTCNNK NNKNNKNNKN NKNNKACCAC CCACATCCGC ACCCAC | 60 66 |
| (2) INFORMATION FOR SEQ ID NO:12: | |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 66 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear | , |
| (ii) MOLECULE TYPE: Genomic DNA | |
| (vii) IMMEDIATE SOURCE: (B) CLONE: AFI6rb | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12: | |
| CTGGCCTGTG TGGATGCGGA TATGMNNMNN MNNMNNMNNC GAMNNAGAAA AGCGGCGATC GCAGGA | 60 66 |
| (2) INFORMATION FOR SEQ ID NO:13: | |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear | |
| (ii) MOLECULE TYPE: Genomic DNA | |
| (vii) IMMEDIATE SOURCE: (B) CLONE: ZFIF | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13: | |
| CATATCCGCA TCCACACAGG CCAG | 24 |
| (2) INFORMATION FOR SEQ ID NO:14: | |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 8 amino acids | |

- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Arg Ser Asp Glu Leu Thr Arg His

- (2) INFORMATION FOR SEQ ID NO:15:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Ser Arg Ser Asp His Leu

- (2) INFORMATION FOR SEQ ID NO:16:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGTAAATGGG CGCCCTTTTG GGCGCCCATT TACG

- (2) INFORMATION FOR SEQ ID NO:17:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Arg Ser Asp Glu Arg Lys Arg His

- (2) INFORMATION FOR SEQ ID NO:18:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:
- Trp Ser Ile Pro Val Leu Leu His
 - (2) INFORMATION FOR SEQ ID NO:19:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Trp Ser Leu Leu Pro Val Leu His

- (2) INFORMATION FOR SEQ ID NO:20:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Phe Ser Phe Leu Leu Pro Leu His

- (2) INFORMATION FOR SEQ ID NO:21:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Leu Ser Thr Trp Arg Gly Trp His

- (2) INFORMATION FOR SEQ ID NO:22:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Thr Ser Ile Gln Leu Pro Tyr His

- (2) INFORMATION FOR SEQ ID NO:23:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 61 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TGATCTCAGA AGCCAAGCAG GGTCGGGCCT GGTTAGTACT TGGATGGGAG ACCGCCTGGG

60 61

- (2) INFORMATION FOR SEQ ID NO:24:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Tyr Ile Cys Ser Phe Ala Asp Cys Gly Ala Ala Tyr Asn Lys Asn Trp

1 5 10

Lys Leu Gln Ala His Leu Cys Lys His Thr

20 25

- (2) INFORMATION FOR SEQ ID NO:25:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Phe Pro Cys Lys Glu Glu Gly Cys Glu Lys Gly Phe Thr Ser Leu His

1 5 10 15

His Leu Thr Arg His Ser Leu Thr His Thr
20 25

- (2) INFORMATION FOR SEQ ID NO:26:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Phe Thr Cys Asp Ser Asp Gly Cys Asp Leu Arg Phe Thr Thr Lys Ala
1 5 10 15

Asn Met Lys Lys His Phe Asn Arg Phe His
20 25

| (2) INFORMATION FOR SEQ ID NO:27: | |
|--|----|
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 13 bas pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear | |
| (ii) MOLECULE TYPE: Genomic DNA | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27: | |
| TGGATGGGAG ACC | 13 |
| (2) INFORMATION FOR SEQ ID NO:28: | |
| (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 8 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear | |
| (ii) MOLECULE TYPE: peptide | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28: | |
| Arg Ser Asp Glu Arg Lys Arg His 1 5 | |
| (2) INFORMATION FOR SEQ ID NO:29: | : |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear | |
| (ii) MOLECULE TYPE: Genomic DNA | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29: | |
| GTCCATAAGA TTAGCGGATC C | 21 |
| (2) INFORMATION FOR SEQ ID NO:30: | |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear | |
| (ii) MOLECULE TYPE: Genomic DNA | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30: | |
| GTGAGCGAGG AAGCGGAAGA G | 21 |
| (2) INFORMATION FOR SEQ ID NO:31: | |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 34 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single | |

| (ii) MOLECULE TYPE: Genomic DNA |
|---|
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31: |
| CCTGCGTGGG CGCCCTTTTG GGCGCCCACG CAGG |
| (2) INFORMATION FOR SEQ ID NO:32: |
| (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 4 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear |
| (ii) MOLECULE TYPE: peptide |
| <pre>(ix) FEATURE: (B) LOCATION: 44 (D) OTHER INFORMATION: where Xaa at position 4 is Lys or Pro</pre> |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32: |
| Thr Gly Glu Xaa |
| 1 (2) INFORMATION FOR SEQ ID NO:33: |
| |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 462 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear |
| (ii) MOLECULE TYPE: Genomic DNA |
| <pre>(ix) FEATURE: (A) NAME/KEY: Coding Sequence (B) LOCATION: 1459</pre> |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33: |
| ATG CTC GAG CTC CCC TAT GCT TGC CCT GTC GAG TCC TGC GAT CGC CGC Met Leu Glu Leu Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg 1 5 10 15 |
| TTT TCT CGC TCG GAT GAG CTT ACC CGC CAT ATC CGC ATC CAC ACA GGC Phe Ser Arg Ser Asp Glu Leu Thr Arg His Ile Arg Ile His Thr Gly 20 25 30 |
| CAG AAG CCC TTC CAG TGT CGA ATA TGC ATG CGT AAC TTC AGT CGT AGT Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser 35 40 45 |
| GAC CAC CTT ACC ACC CAC ATC CGC ACC CAC ACA GGC GAG AAG CCT TTT Asp His Leu Thr Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe 50 55 60 |
| GCC TGT GAC ATT TGT GGG AGG AAG TTT GCC AGG AGT GAT GAA CGC AAG Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys 65 70 75 80 |
| AGG CAT ACC AAA ATC CAT ACC GGR CAG AAG CCC ACT AGT GGC GGT GGT Arg His Thr Lys Ile His Thr Xaa Gln Lys Pro Thr Ser Gly Gly 85 90 95 |

| CGG Arg | ATC Ile | GCC Ala | CGG Arg 100 | CTG Leu | GAG Glu | GAA Glu | AAA Lys | GTG Val 105 | AAA Lys | ACC Thr | TTG Leu | AAA Lys | GCG Ala 110 | CAA Gln | AAC Asn | 336 |
|------------|-------------------|-------------------|-------------------|------------|-------------------|-------------------|-------------------|-------------------|------------|------------|-------------------|-------------------|-------------------|------------|------------|-----|
| TCC Ser | GAG Glu | CTG Leu 115 | GCG Ala | TCC Ser | ACC Thr | CGG Arg | AAC Asn 120 | ATG Met | CTC Leu | AGG Arg | GAA Glu | CAG Gln 125 | GTG Val | GCA Ala | CAG Gln | 384 |
| CTT Leu | AAA Lys 130 | CAG Gln | AAA Lys | GTC Val | ATG Met | AAC Asn 135 | CAC His | GCT Ala | AGC Ser | GGC Gly | CAG Gln 140 | GCC Ala | GGC Gly | CAG Gln | TAC Tyr | 432 |
| | | | | | GAC Asp 150 | | | | TAA | | | | | | | 462 |

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 153 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Leu Glu Leu Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg 10 Phe Ser Arg Ser Asp Glu Leu Thr Arg His Ile Arg Ile His Thr Gly 25 20 Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser 40 Asp His Leu Thr Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe 60 55 Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys 70 Arg His Thr Lys Ile His Thr Xaa Gln Lys Pro Thr Ser Gly Gly 90 Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu Lys Ala Gln Asn 105 100 Ser Glu Leu Ala Ser Thr Arg Asn Met Leu Arg Glu Gln Val Ala Gln 120 125 115 Leu Lys Gln Lys Val Met Asn His Ala Ser Gly Gln Ala Gly Gln Tyr 140 135 130 Pro Tyr Asp Val Pro Asp Tyr Ala Ser 150 145

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 462 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 1...459

145

| | (ж | i) S | EQUE | NCE | DESC | RIPT | : NOI: | SEÇ | מז נ | NO: 3 | | | | | | |
|------------------|-------------------|-------------------|-------------------|------------------|------------------|-------------------|-------------------|-------------------|------------------|------------------|-------------------|-------------------|-------------------|------------------|------------------|-----|
| ATG Met 1 | CTC Leu | GAG Glu | CTC Leu | CCC Pro 5 | TAT Tyr | GCT Ala | TGC Cys | CCT Pro | GTC Val 10 | GAG Glu | TCC Ser | TGC Cys | GAT Asp | CGC Arg 15 | CGC Arg | 48 |
| TTT Phe | TCT Ser | CGC Arg | TCG Ser 20 | GAT Asp | GAG Glu | CTT Leu | ACC Thr | CGC Arg 25 | CAT His | ATC Ile | CGC Arg | ATC Ile | CAC His 30 | ACA Thr | GGC Gly | 96 |
| CAG Gln | AAG Lys | CCC Pro 35 | TTC Phe | CAG Gln | TGT Cys | CGA Arg | ATA Ile 40 | TGC Cys | ATG Met | CGT Arg | AAC Asn | TTC Phe 45 | AGT Ser | CGT Arg | AGT Ser | 144 |
| GAC Asp | CAC His 50 | CTT Leu | ACC Thr | ACC Thr | CAC His | ATC Ile 55 | CGC Arg | ACC Thr | CAC His | ACA Thr | GGC Gly 60 | GAG Glu | AAG Lys | CCT Pro | TTT Phe | 192 |
| GCC Ala 65 | TGT Cys | GAC Asp | ATT Ile | TGT Cys | GGG Gly 70 | AGG Arg | AAG Lys | TTT Phe | GCC Ala | AGG Arg 75 | AGT Ser | GAT Asp | GAA Glu | CGC Arg | AAG Lys 80 | 240 |
| AGG Arg | CAT His | ACC Thr | AAA Lys | ATC Ile 85 | CAT His | ACC Thr | GGT Gly | CAG Gln | AAG Lys 90 | CCC Pro | ACT Thr | AGT Ser | GGC Gly | GGT Gly 95 | GGT Gly | 288 |
| CTG Leu | ACC Thr | GAC Asp | ACC Thr 100 | CTG Leu | CAG Gln | GCG Ala | GAA Glu | ACC Thr 105 | GAC Asp | CAG Gln | CTG Leu | GAA Glu | GAC Asp 110 | GAA Glu | AAA Lys | 336 |
| TCC | GCG Ala | CTG Leu 115 | CAA Gln | ACC Thr | GAA Glu | ATC Ile | GCG Ala 120 | Asn | CTG Leu | CTG Leu | AAA Lys | GAA Glu 125 | Lys | GAA Glu | AAG Lys | 384 |
| CTG Leu | GAG Glu 130 | Phe | ATC Ile | CTG Leu | GCG Ala | GCA Ala 135 | His | GCT Ala | AGC Ser | GGC Gly | CAG Gln 140 | Ala | GGC Gly | CAG Gln | TAC Tyr | 432 |
| | TAC | | | | | | | | | | | | | | | 46 |

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 153 amino acids

150

- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

 Met
 Leu
 Glu
 Leu
 Pro
 Tyr
 Ala
 Cys
 Pro
 Val
 Glu
 Ser
 Cys
 Arg
 Arg
 Inches
 Inch

Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys 65 70 75 80

Arg His Thr Lys Ile His Thr Gly Gln Lys Pro Thr Ser Gly Gly Gly 85 90 95

Leu Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys 100

Ser Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys 115

Leu Glu Phe Ile Leu Ala Ala His Ala Ser Gly Gln Ala Gly Gln Tyr 130

Pro Tyr Asp Val Pro Asp Tyr Ala Ser 150

- (2) INFORMATION FOR SEQ ID NO:37:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CGCCCACGCN GCGTGGGCG

19

- (2) INFORMATION FOR SEQ ID NO:38:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CGCCCACGCN GCGGCGGCG CGGCGGCG

28

- (2) INFORMATION FOR SEQ ID NO:39:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 76 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (B) LOCATION: 76...76
- (D) OTHER INFORMATION: where Xaa at position 76 is Tyr-Ala-Cys-Pro-Val-Glu-Ser-Cys-Asp-Arg-Phe-Ser-Lys-Ser-Ala-Asp-Leu-Lys-His-Ile-Arg-His-Thr-Gly-Glu-Lys-Pro-Met-Lys-Leu-Leu-Glu-Pro-repeated 10 times; residue 76=340 amino acids; some Xaa's may be missing
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met Lys Leu Leu Glu Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg
1 5 10 15

Arg Phe Ser Lys Ser Ala Asp Leu Lys Arg His Ile Arg His Thr Gly
20 25 30

Glu Lys Pro Met Lys Leu Leu Glu Pro Tyr Ala Cys Pro Val Glu Ser 40 Cys Asp Arg Arg Phe Ser Lys Ser Ala Asp Leu Lys His Ile Arg His 55 Thr Gly Glu Lys Pro Met Lys Leu Leu Glu Pro Xaa 70 (2) INFORMATION FOR SEQ ID NO:40: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 34 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: Genomic DNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40: 34 CCTCGCCGCC GCGGGTTTTC CCGCGCCCCC GAGG (2) INFORMATION FOR SEQ ID NO:41: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 293 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: Genomic DNA (ix) FEATURE: (A) NAME/KEY: Coding Sequence (B) LOCATION: 1...294 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41: ATG AAA CTG CTC GAG CCC TAT GCT TGC CCT GTC GAG TCC TGC GAT CGC 48 Met Lys Leu Leu Glu Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg CGC TTT TCT AAG TCG GCT GAT CTG AAG CGC CAT ATC CGC ATC CAC ACT 96 Arg Phe Ser Lys Ser Ala Asp Leu Lys Arg His Ile Arg Ile His Thr GGC GAA AAA CCG TAC GCG TGC CCT GTC GAG TCC TGC GAT CGC CGC TTT 144 Gly Glu Lys Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe TCT AAG TCG GCT GAT CTG AAG CGC CAT ATC CGC ATC CAC ACC GGG GAG 192 Ser Lys Ser Ala Asp Leu Lys Arg His Ile Arg Ile His Thr Gly Glu 55 AAG CCC TAT GCT TGC CCT GTC GAG TCC TGC GAT CGC CGC TTT TCT AAG 240

Lys Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Lys

TCG GCT GAT CTG AAG CGC CAT ATC CGC ATC CAC ACC GGT CAG AAG CCC

Ser Ala Asp Leu Lys Arg His Ile Arg Ile His Thr Gly Gln Lys Pro

70

85

ACT AC Thr Thr 293

288



(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

 Met
 Lys
 Leu
 Leu
 Glu
 Pro
 Tyr
 Ala
 Cys
 Pro
 Val
 Glu
 Ser
 Cys
 Asp
 Leu
 Lys
 Arg
 His
 Ile
 Arg
 Ile
 His
 Thr

 Gly
 Glu
 Lys
 Pro
 Tyr
 Ala
 Cys
 Pro
 Val
 Glu
 Ser
 Cys
 Asp
 Arg
 Phe

 Ser
 Lys
 Ser
 Ala
 Asp
 Leu
 Lys
 Arg
 His
 Ile
 Arg
 Arg
 Arg
 Phe

 Lys
 Pro
 Tyr
 Ala
 Cys
 Pro
 Val
 Glu
 Ser
 Cys
 Asp
 Arg
 Phe
 Ser
 Lys
 Arg
 His
 Ile
 His
 Thr
 Glu
 Ser
 Lys
 Arg
 Phe
 Ser
 Lys
 Arg
 His
 Ile
 His
 Thr
 Glu
 Ser
 Lys
 Arg
 His
 Thr
 Glu
 Thr
 Glu

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 543 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 1...543
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

| ATG Met 1 | CTC Leu | GAG Glu | CTC Leu | CCC Pro 5 | TAT Tyr | GCT Ala | TGC Cys | CCT Pro | GTC Val 10 | GAG Glu | TCC Ser | TGC Cys | GAT Asp | CGC Arg 15 | CGC Arg | 48 |
|------------------|------------------|------------------|------------------|-----------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|-----|
| TTT Phe | TCT Ser | CGC Arg | TCG Ser 20 | GAT Asp | GAG Glu | CTT Leu | ACC Thr | CGC Arg 25 | CAT His | ATC Ile | CGC Arg | ATC Ile | CAC His 30 | ACA Thr | GGC Gly | 96 |
| CAG Gln | AAG Lys | CCC Pro 35 | TTC Phe | CAG Gln | TGT Cys | CGA Arg | ATA Ile 40 | TGC Cys | ATG Met | CGT Arg | AAC Asn | TTC Phe 45 | AGT Ser | CGT Arg | AGT Ser | 144 |
| GAC Asp | CAC His 50 | Leu | ACC Thr | ACC Thr | CAC His | ATC Ile 55 | CGC Arg | ACC Thr | CAC His | ACA Thr | GGC Gly 60 | GAG Glu | AAG Lys | CCT Pro | TTT Phe | 192 |
| GCC Ala 65 | Сув | GAC Asp | ATT Ile | TGT Cys | GGG Gly 70 | AGG Arg | AAG Lys | TTT Phe | GCC Ala | AGG Arg 75 | AGT Ser | GAT Asp | GAA Glu | CGC Arg | AAG Lys 80 | 240 |

| | | | | | | | | | | | | | | _ | | |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------|
| AGG Arg | CAT His | ACC Thr | AAA Lys | ATC Ile 85 | CAT His | ACC Thr | GGG Gly | GAG Glu | AAG Lys 90 | CCC Pro | TAT Tyr | GCT Ala | TGC Cys | CCT Pro 95 | GTC Val | 288 |
| GAG Glu | TCC Ser | TGC Cys | GAT Asp 100 | CGC Arg | CGC Arg | TTT Phe | TCT Ser | CGC Arg 105 | TCG Ser | GAT Asp | GAG Glu | CTT Leu | ACC Thr 110 | CGC Arg | CAT His | 336 |
| ATC Ile | CGC Arg | ATC Ile 115 | CAC His | ACA Thr | GGC Gly | CAG Gln | AAG Lys 120 | CCC Pro | TTC Phe | CAG Gln | TGT Cys | CGA Arg 125 | ATA Ile | TCC Ser | ATG Met | 384 |
| CGT Arg | AAC Asn 130 | TTC Phe | AGT Ser | CGT Arg | AGT Ser | GAC Asp 135 | CAC His | CTT Leu | ACC Thr | ACC Thr | CAC His 140 | ATC Ile | CGC Arg | ACC Thr | CAC His | 432 |
| ACA Thr 145 | GGC Gly | GAG Glu | AAG Lys | CCT Pro | TTT Phe 150 | GCC Ala | TGT Cys | Asp | ATT Ile | TGT Cys 155 | GGG Gly | AGG Arg | AAG Lys | TTT Phe | GCC Ala 160 | 4 80 |
| AGG Arg | AGT Ser | GAT Asp | GAA Glu | CGC Arg 165 | AAG Lys | AGG Arg | CAT His | ACC Thr | AAA Lys 170 | ATC Ile | CAT His | TTA Leu | AGA Arg | CAG Gln 175 | AAG Lys | 528 |
| | TCT Ser | | | Ser | | | | | | | | | | | | 543 |

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 181 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Met Leu Glu Leu Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg 1 10 Phe Ser Arg Ser Asp Glu Leu Thr Arg His Ile Arg Ile His Thr Gly 25 20 Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser 40 35 Asp His Leu Thr Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe 60 55 Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys 70 Arg His Thr Lys Ile His Thr Gly Glu Lys Pro Tyr Ala Cys Pro Val 95 90 Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser Asp Glu Leu Thr Arg His 110 105 100 Ile Arg Ile His Thr Gly Gln Lys Pro Phe Gln Cys Arg Ile Ser Met 125 120 115 Arg Asn Phe Ser Arg Ser Asp His Leu Thr Thr His Ile Arg Thr His 140 135 130 Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala 155 150 Arg Ser Asp Glu Arg Lys Arg His Thr Lys Ile His Leu Arg Gln Lys 175 170 165

Asp Ser Arg Thr Ser 180 (2). INFORMATION FOR SEQ ID NO:45: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 46 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: Genomic DNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45: GAGGAGGAGG AGGGATCCAT GCTCGAGCTC CCCTATGCTT GCCCTG

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs

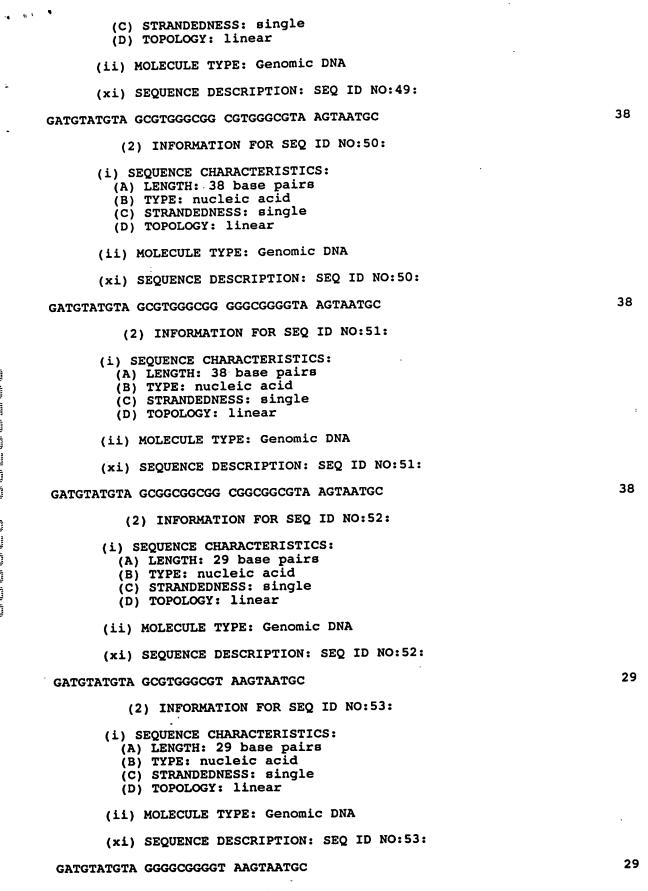
 - (B) TYPE: nucleic acid (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:
- GAGGAGGAGA CCGGTATGGA TTTTGGTATG CCTCTTGCG
 - (2) INFORMATION FOR SEQ ID NO:47:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Genomic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47: GAGGAGGAGA CCGGTGAGAA GCCCTATGCT TGCCCTGTCG AGTCCTGCGA TCGCCGC
 - (2) INFORMATION FOR SEQ ID NO:48:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Genomic DNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:
- GAGGAGGAGA CTAGTTCTAG AGTCCTTCTG TC
 - (2) INFORMATION FOR SEQ ID NO:49:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid

32

57

46

39:



| , | (2) INFORMATION FOR SEQ ID NO:54: | |
|---|--|----|
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 29 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear | |
| | (ii) MOLECULE TYPE: Genomic DNA | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54: | |
| | GATGTATGTA GCGTGGGCGT AAGTAATGC | 29 |
| | (2) INFORMATION FOR SEQ ID NO:55: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 41 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear | |
| | (ii) MOLECULE TYPE: Genomic DNA | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55: | |
| | GAGGAGGAGG AATTCCGACA TTTATAATGA ACGTGAATTG C | 41 |
| | (2) INFORMATION FOR SEQ ID NO:56: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 45 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear | |
| | (ii) MOLECULE TYPE: Genomic DNA | • |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56: | |
| | TGCGCCCACG CCGCCCACGC GATGATTGGG AGCTTTTTTT GCACG | 45 |
| | (2) INFORMATION FOR SEQ ID NO:57: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 51 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear | |
| | (ii) MOLECULE TYPE: Genomic DNA | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57: | • |
| | TCGCGTGGGC GGCGTGGGCG CAAAAAATTA TTATCATGGA TTCTAAAACG G | 51 |
| | (2) INFORMATION FOR SEQ ID NO:58: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 42 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear | |

| gi C 1 | |
|--|---------|
| (ii) MOLECULE TYPE: Genomic DNA | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58: | |
| GAGGAGGAGG CGGCCGCAGG TAGATGAGAT GTGACGAACG TG | 42 |
| (2) INFORMATION FOR SEQ ID NO:59: | |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 45 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear | |
| (ii) MOLECULE TYPE: Genomic DNA | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59: | |
| TGCCCCGCCC CCGCCCACGC GATGATTGGG AGCTTTTTTT GCACG | 45 |
| (2) INFORMATION FOR SEQ ID NO:60: | |
| (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 51 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear | |
| (ii) MOLECULE TYPE: Genomic DNA | ·; |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60: | - Caral |
| TCGCGTGGGC GGGGCGGGG CAAAAAATTA TTATCATGGA TTCTAAAACG G | 51 |
| (2) INFORMATION FOR SEQ ID NO:61: | |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear | |
| (ii) MOLECULE TYPE: Genomic DNA | |
| (x1) SEQUENCE DESCRIPTION: SEQ ID NO:61: | |
| GCGTGGGCGG CGTGGGCG | 18 |
| (2) INFORMATION FOR SEQ ID NO:62: | |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear | |
| (ii) MOLECULE TYPE: Genomic DNA | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62: | |
| GCGTGGGCGG GGGCGGGG | 18 |
| | |